

2590  
2508 #5



OIEP

## RAW SEQUENCE LISTING

DATE: 05/02/2002

PATENT APPLICATION: US/10/024,066

TIME: 14:18:08

Input Set : A:\IU-98us1.APP

Output Set: N:\CRF3\05022002\J024066.raw

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3 <110> APPLICANT: Field, Loren J.
4   Pasumarthi, Kishore Babu S.
6 <120> TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
7   AND METHODS FOR PREPARING AND USING SAME
9 <130> FILE REFERENCE: 7037-450
11 <140> CURRENT APPLICATION NUMBER: 10/024,066
12 <141> CURRENT FILING DATE: 2001-12-18
14 <150> PRIOR APPLICATION NUMBER: 60/139,942
15 <151> PRIOR FILING DATE: 1999-06-18
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/16827
18 <151> PRIOR FILING DATE: 2000-06-19
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 876
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (4)..(870)
33 <400> SEQUENCE: 1
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38 ccg gac cgc aac ctg ctg gaa gac cgc gtt ctg cag aac ctg ttg acc   96
39 Pro Asp Arg Asn Leu Leu Glu Asp Arg Val Leu Gln Asn Leu Leu Thr
40     20             25             30
42 atc gag gag cgc tac ctc ccg cag tgt tcc tat ttc aag tgc gtg cag   144
43 Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln
44     35             40             45
46 aag gac atc caa ccg tac atg cgc agg atg gtg gcc acc tgg atg cta   192
47 Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu
48     50             55             60
50 gag gtc tgt gag gaa caa aag tgt gaa gaa gag gtc ttt cct ctg gcc   240
51 Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu Ala
52     65             70             75
54 atg aat tac ctg gac cgt ttc ttg gct gga gtc ccg act cct aag acc   288
55 Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Thr
56  80             85             90             95
58 cat ctt cag ctc ctg ggt gca gtg tgc atg ttc cta gct tcc aag ctg   336
59 His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu
60     100            105            110
62 aaa gag acc atc ccg ctg act gcg gaa aag ctg tgc att tac acc gac   384

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63 Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp
64      115      120      125
66 aac tct gtg aag ccc cag gag ctg ctg gag tgg gaa ctg gta gtg ttg 432
67 Asn Ser Val Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu
68      130      135      140
70 ggt aag ctg aag tgg aac ctg gcc gca gtc acc cct cac gac ttc att 480
71 Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile
72      145      150      155
74 gag cac atc ctt cgc aag ctg ccc cag caa aag gag aag ctg tcc ctg 528
75 Glu His Ile Leu Arg Lys Leu Pro Gln Gln Lys Glu Lys Leu Ser Leu
76 160      165      170      175
78 atc cgc aag cat gcg cag acc ttc atc gct ctg tgc gct acc gac ttc 576
79 Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe
80      180      185      190
82 aag ttt gcc atg tac ccg cca tcg atg att gca act gga agc gtg gga 624
83 Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly
84      195      200      205
86 gca gcc atc tgt ggg ctt cag cag gat gat gaa gtg aac aca ctc acg 672
87 Ala Ala Ile Cys Gly Leu Gln Gln Asp Asp Glu Val Asn Thr Leu Thr
88      210      215      220
90 tgt gat gcc ctg act gag ctg ctg gcc aag atc acc cac act gat gtg 720
91 Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr His Thr Asp Val
92      225      230      235
94 gat tgt ctc aaa gcc tgc cag gag caa atc gaa gct ctg ctg ctg aac 768
95 Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Leu Asn
96 240      245      250      255
98 agc ctg cag cag ttc cgt caa gag cag cat aac gcc gga tcc aag tct 816
99 Ser Leu Gln Gln Phe Arg Gln Glu Gln His Asn Ala Gly Ser Lys Ser
100      260      265      270
102 gtg gaa gat ccg gac caa gcc acc acc cct aca gac gtg cgg gat gtt 864
103 Val Glu Asp Pro Asp Gln Ala Thr Thr Pro Thr Asp Val Arg Asp Val
104      275      280      285
106 gac ctg tgagga 876
107 Asp Leu
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 289
112 <212> TYPE: PRT
113 <213> ORGANISM: Mus musculus
115 <400> SEQUENCE: 2
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117 1 5 10 15
119 Asp Arg Asn Leu Leu Glu Asp Arg Val Leu Gln Asn Leu Leu Thr Ile
120 20 25 30
122 Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln Lys
123 35 40 45
125 Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu Glu
126 50 55 60
128 Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu Ala Met
129 65 70 75 80

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131 Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Thr His
132      85                      90                      95
134 Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu Lys
135      100                      105                      110
137 Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp Asn
138      115                      120                      125
140 Ser Val Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu Gly
141      130                      135                      140
143 Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile Glu
144 145                      150                      155                      160
146 His Ile Leu Arg Lys Leu Pro Gln Gln Lys Glu Lys Leu Ser Leu Ile
147      165                      170                      175
149 Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe Lys
150      180                      185                      190
152 Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly Ala
153      195                      200                      205
155 Ala Ile Cys Gly Leu Gln Gln Asp Asp Glu Val Asn Thr Leu Thr Cys
156      210                      215                      220
158 Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr His Thr Asp Val Asp
159 225                      230                      235                      240
161 Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Leu Asn Ser
162      245                      250                      255
164 Leu Gln Gln Phe Arg Gln Glu Gln His Asn Ala Gly Ser Lys Ser Val
165      260                      265                      270
167 Glu Asp Pro Asp Gln Ala Thr Thr Pro Thr Asp Val Arg Asp Val Asp
168      275                      280                      285
170 Leu
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176 <211> LENGTH: 873
177 <212> TYPE: DNA
178 <213> ORGANISM: Homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (4)..(870)
184 <400> SEQUENCE: 3
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187      1                      5                      10                      15
189 cgg gac cgc aac ctg ctc cga gac gac cgc gtc ctg cag aac ctg ctc 96
190 Arg Asp Arg Asn Leu Leu Arg Asp Asp Arg Val Leu Gln Asn Leu Leu
191      20                      25                      30
193 acc atc gag gag cgc tac ctt ccg cag tgc tcc tac ttc aag tgc gtg 144
194 Thr Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val
195      35                      40                      45
197 cag aag gac atc caa ccc tac atg cgc aga atg gtg gcc acc tgg atg 192
198 Gln Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met
199      50                      55                      60
201 ctg gag gtc tgt gag gaa cag aag tgc gaa gaa gag gtc ttc cct ctg 240
202 Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu

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203      65      70      75
205 gcc atg aat tac ctg gac cgt ttc ttg gct ggg gtc ccg act ccg aag 288
206 Ala Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys
207 80      85      90      95
209 tcc cat ctg caa ctc ctg ggt gct gtc tgc atg ttc ctg gcc tcc aaa 336
210 Ser His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys
211      100      105      110
213 ctc aaa gag acc agc ccg ctg acc gcg gag aag ctg tgc att tac acc 384
214 Leu Lys Glu Thr Ser Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr
215      115      120      125
217 gac aac tcc atc aag cct cag gag ctg ctg gag tgg gaa ctg gtg gtg 432
218 Asp Asn Ser Ile Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val
219      130      135      140
221 ctg ggg aag ttg aag tgg aac ctg gca gct gtc act cct cat gac ttc 480
222 Leu Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe
223      145      150      155
225 att gag cac atc ttg cgc aag ctg ccc cag cag cgg gag aag ctg tct 528
226 Ile Glu His Ile Leu Arg Lys Leu Pro Gln Gln Arg Glu Lys Leu Ser
227 160      165      170      175
229 ctg atc cgc aag cat gct cag acc ttc att gct ctg tgt gcc acc gac 576
230 Leu Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp
231      180      185      190
233 ttt aag ttt gcc atg tac cca ccg tcg atg atc gca act gga agt gtg 624
234 Phe Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val
235      195      200      205
237 gga gca gcc atc tgt ggg ctc cag cag gat gag gaa gtg agc tcg ctc 672
238 Gly Ala Ala Ile Cys Gly Leu Gln Gln Asp Glu Glu Val Ser Ser Leu
239      210      215      220
241 act tgt gat gcc ctg act gag ctg ctg gct aag atc acc aac aca gac 720
242 Thr Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr Asn Thr Asp
243      225      230      235
245 gtg gat tgt ctc aaa gct tgc cag gag cag att gag gcg gtg ctc ctc 768
246 Val Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Val Leu Leu
247 240      245      250      255
249 aat agc ctg cag cag tac cgt cag gac caa cgt gac gga tcc aag tcg 816
250 Asn Ser Leu Gln Gln Tyr Arg Gln Asp Gln Arg Asp Gly Ser Lys Ser
251      260      265      270
253 gag gat gaa ctg gac caa gcc agc acc cct aca gac gtg cgg gat atc 864
254 Glu Asp Glu Leu Asp Gln Ala Ser Thr Pro Thr Asp Val Arg Asp Ile
255      275      280      285
257 gac ctg tga 873
258 Asp Leu
261 <210> SEQ ID NO: 4
262 <211> LENGTH: 289
263 <212> TYPE: PRT
264 <213> ORGANISM: Homo sapiens
266 <400> SEQUENCE: 4
267 Met Glu Leu Leu Cys His Glu Val Asp Pro Val Arg Arg Ala Val Arg
268 1      5      10      15

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270 Asp Arg Asn Leu Leu Arg Asp Asp Arg Val Leu Gln Asn Leu Leu Thr
271           20                25                30
273 Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln
274           35                40                45
276 Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu
277           50                55                60
279 Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu Ala
280           65                70                75                80
282 Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Ser
283           85                90                95
285 His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu
286           100               105               110
288 Lys Glu Thr Ser Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp
289           115               120               125
291 Asn Ser Ile Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu
292           130               135               140
294 Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile
295           145               150               155               160
297 Glu His Ile Leu Arg Lys Leu Pro Gln Gln Arg Glu Lys Leu Ser Leu
298           165               170               175
300 Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe
301           180               185               190
303 Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly
304           195               200               205
306 Ala Ala Ile Cys Gly Leu Gln Gln Asp Glu Glu Val Ser Ser Leu Thr
307           210               215               220
309 Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr Asn Thr Asp Val
310           225               230               235               240
312 Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Val Leu Leu Asn
313           245               250               255
315 Ser Leu Gln Gln Tyr Arg Gln Asp Gln Arg Asp Gly Ser Lys Ser Glu
316           260               265               270
318 Asp Glu Leu Asp Gln Ala Ser Thr Pro Thr Asp Val Arg Asp Ile Asp
319           275               280               285
321 Leu

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326 &lt;210&gt; SEQ ID NO: 5

327 &lt;211&gt; LENGTH: 5443

328 &lt;212&gt; TYPE: DNA

329 &lt;213&gt; ORGANISM: Mus musculus

331 &lt;400&gt; SEQUENCE: 5

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334 ttcaaaaggg cctgaatgag gagtagatct tgtgctaccc agctctaagg gtgcccggtga 180
335 agccctcaga cctggagcct ttgcaacagc ccttttaggtg gaagcagaat aaagcaattt 240
336 tccttaaagc caaaatcctg cctctagact cttcttctct gacctcggtc cctgggctct 300
337 aggggtgggga ggtggggcctt ggaagaagaa ggtggggaag tggcaaaagc cgatccctag 360
338 ggccctgtga agttcggagc cttccctgta cagcactggc tcatagatcc tcctccagcc 420
339 aaacatagca agaagtgata cctcctttgt gacttccccca ggcccagtac ctgtcagggt 480
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/024,066

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